PI 1183772

THE UNITED STATES OF AMERICA

TO ALL TO WHOM THESE PRESENTS SHALL COME:

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office

June 17, 2004

THIS IS TO CERTIFY THAT ANNEXED HERETO IS A TRUE COPY FROM THE RECORDS OF THE UNITED STATES PATENT AND TRADEMARK OFFICE OF THOSE PAPERS OF THE BELOW IDENTIFIED PATENT APPLICATION THAT MET THE REQUIREMENTS TO BE GRANTED A FILING DATE.

APPLICATION NUMBER: *60/462,989*
FILING DATE: *April 14, 2003*
RELATED PCT APPLICATION NUMBER: *PCT/US04/11533*

By Authority of the
COMMISSIONER OF PATENTS AND TRADEMARKS

N. WOODSON
Certifying Officer

PRIORITY DOCUMENT
SUBMITTED OR TRANSMITTED IN COMPLIANCE WITH RULE 17.1(a) OR (b)

04-16-03 60462989 .04

Please type a plus sign (+) inside this box → [+]

PTO/SB/16 (02-01)
Approved for use through 10/31/2002. OMB 0651-0032
U.S. Patent and Trademark Office: U.S. DEPARTMENT OF COMMERCE
Under the Paperwork Reduction Act of 1995, no persons are required to respond to a collection of information unless it displays a valid OMB control number.

PROVISIONAL APPLICATION FOR PATENT COVER SHEET

This is a request for filing a PROVISIONAL APPLICATION FOR PATENT under 37 CFR 1.53(c).

Express Mail Label No. EL 852 434 344 US

INVENTOR(S)		
Given Name (first and middle [if any])	Family Name or Surname	Residence (City and either State or Foreign Country)
M. Bishr Nam-On	Omary Ku	Palo Alto, California Palo Alto, California

☐ Additional inventors are being named on the separately numbered sheets attached hereto

TITLE OF THE INVENTION (280 characters max)

KERATIN 8 AND 18 MUTATIONS ARE RISK FACTORS FOR DEVELOPING LIVER DISEASE OF MULTIPLE ETIOLOGIES

Direct all correspondence to: **CORRESPONDENCE ADDRESS**

☒ Customer Number 24353 →

OR Type Customer Number here

Place Customer Number Bar Code Label here

☐ Firm or Individual Name	Bozicevic, Field & Francis LLP				
Address	200 Middlefield Road, Suite 200				
Address					
City	Menlo Park	State	California	Zip	94025
Country	U.S.A.	Telephone	(650) 327-3400	Fax	(650) 327-3231

ENCLOSED APPLICATION PARTS (check all that apply)

☒ Specification Number of Pages 27
☒ Drawing(s) Number of Sheets 2
☒ Application Data Sheet. See 37 CFR 1.76
☐ CD(s), Number
☒ Other (specify) Application Data Sheet, Postcard

METHOD OF PAYMENT OF FILING FEES FOR THIS PROVISIONAL APPLICATION FOR PATENT

☒ Applicant claims small entity status. See 37 CFR 1.27.
☐ A check or money order is enclosed to cover the filing fees
☒ The Commissioner is hereby authorized to charge filing fees or credit any overpayment to Deposit Account Number: 50-0815
☐ Payment by credit card. Form PTO-2038 is attached.

FILING FEE AMOUNT$ 80.00

The invention was made by an agency of the United States Government or under a contract with an agency of the United States Government.

☒ No
☐ Yes, the name of the U.S. Government agency and the Government contract number are: _____

Respectfully submitted,

SIGNATURE Pamela Sherwood Date 04/14/2003

TYPED or PRINTED NAME Pamela J. Sherwood REGISTRATION NO. (if appropriate) 36,677

TELEPHONE (650) 327-3400 Docket Number: STAN-297PRV

USE ONLY FOR FILING A PROVISIONAL APPLICATION FOR PATENT

This collection of information is required by 37 CFR 1.51. The information is used by the public to file (and by the PTO to process) a provisional application. Confidentiality is governed by 35 U.S.C. 122 and 37 CFR 1.14. This collection is estimated to take 8 hours to complete, including gathering, preparing, and submitting the complete provisional application to the PTO. Time will vary depending upon the individual case. Any comments on the amount of time you require to complete this form and/or suggestions for reducing this burden, should be sent to the Chief Information Officer, U.S. Patent and Trademark Office, U.S. Department of Commerce, Washington, D.C. 20231. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO: Box Provisional Application, Assistant Commissioner for Patents, Washington, D.C. 20231.

APPLICATION INFORMATION

Application Type::	Provisional
Title::	KERATIN 8 AND 18 MUTATIONS ARE RISK FACTORS FOR DEVELOPING LIVER DISEASE OF MULTIPLE ETIOLOGIES
Attorney Docket Number::	STAN-297PRV
Request for Non-Publication?::	
Assignee for Publication::	
Total Drawing Sheets::	2
Small Entity?::	Small
License US Govt. Agency::	No
Contract or Grant Numbers::	
Sequence Submission?::	No
Computer Readable Form (CRF)?::	

INVENTOR INFORMATION

Inventor One Given Name::	M. Bishr
Family Name::	Omary
Postal Address Line One::	Palo Alto VA Medical Center
Postal Address Line Two::	Mail Code 154J, 3801 Miranda Avenue
City::	Palo Alto
State or Province::	California
Postal or Zip Code::	94304
Citizenship Country::	
Inventor Two Given Name::	Nam-On
Family Name::	Ku
Postal Address Line One::	
Postal Address Line Two:	
City::	Palo Alto
State or Province::	California
Postal or Zip Code::	
Citizenship Country::	
Inventor Three Given Name::	
Family Name::	
Postal Address Line One::	
Postal Address Line Two::	
City::	
State or Province::	
Postal or Zip Code::	
Citizenship Country::	

[redacted]

CORRESPONDENCE INFORMATION

Correspondence Customer Number::	24353
Telephone One::	(650) 327-3400
Telephone Two::	(650) 833-7790
Fax::	(650) 327-3231
Electronic Mail::	sherwood@bozpat.com

REPRESENTATIVE INFORMATION

Representative Customer Number::	24353

CONTINUITY INFORMATION

This application is a::	Non Prov. Of Provisional...
> Application One::	
Filing Date::	
This application is a::	
> Application Two::	
Filing Date::	
which is a::	
>> Application Three::	
Filing Date::	
which is a::	
>>> Application Four::	
Filing Date::	

PRIOR FOREIGN APPLICATIONS

Foreign Application One::
Filing Date::
Country::
Priority Claimed::

[redacted]

KERATIN 8 AND 18 MUTATIONS ARE RISK FACTORS FOR DEVELOPING LIVER DISEASE OF MULTIPLE ETIOLOGIES

INTRODUCTION

[01] Keratin mutations are associated with several skin, oral, esophageal, ocular and cryptogenic liver diseases that reflect tissue-specific expression of the particular keratin involved. The resulting cellular and tissue defects are manifestations of the clearly defined function of keratins that provides cells with ability to cope with mechanical stresses. This keratin cytoprotective effect is evident in the blistering phenotype of several human keratin skin diseases such as epidermolysis bullosa simplex, and the phenotypes of animal models that lack or express a mutant keratin. Also, emerging evidence suggests that keratins protect cells from nonmechanical forms of injury via several mechanisms that may include: keratin regulation of cell signaling cascades, regulation of the availability of other cellular proteins, and protein targeting to subcellular compartments.

[02] The function of keratins in protecting cells from mechanical stress is related to their unique properties and abundance as one of three major cytoskeletal protein families, which include intermediate filaments (IF), microfilaments and microtubules. Keratins (K) are members of the IF protein family, and are specifically expressed in epithelial cells and their appendages. They consist of >20 members (K1-K20), and are further classified into type I (K9-K20) and type II (K1-K8) keratins which form obligate, noncovalent heteropolymers. Keratins serve as important cell-type-specific markers. For example, unique keratin complements distinguish different epithelial cell types and thereby reflect epithelial subtype-specific diseases that result from keratin-specific mutations. As such, keratinocytes express K5/K14 basally and K1/K10 suprabasally, and hepatocytes express K8/K18. K8/K18 are also found in other glandular cells including enterocytes, with variable complements of K19/K20/K7 depending on the cell type.

[03] Most keratin diseases are autosomal-dominant with near complete penetrance. Exceptions appear to be K18 and K8 mutations in patients with cryptogenic cirrhosis. To date, 6 patients have been described with K8 (5 patients) or K18 (1 patient) mutations, from a group of 55 patients with cryptogenic cirrhosis. Most patients with cryptogenic cirrhosis, including those with K8/K18 mutations, do not have a well-defined liver disease family history. Absence of a clear family history suggests that K8/K18 mutations predispose to, rather than cause, liver disease. The presence and frequency of keratin mutations in noncryptogenic liver disease is heretofore unknown.

SUMMARY OF THE INVENTION

[04] Keratin 8 and 18 (K8/K18) mutations are shown to be associated with a predisposition to liver disease, particularly noncryptogenic liver disease. Unique K8/K18 mutations are shown in patients with diseases including biliary atresia, acute fulminant hepatitis, viral hepatitis B or C, alcoholic liver disease, primary biliary cirrhosis, autoimmune hepatitis, and the like. Livers with keratin mutations had increased incidence of cytoplasmic filamentous deposits. Therefore, K8/K18 are susceptibility genes for developing cryptogenic and noncryptogenic forms of liver disease. Alleles are associated with disease susceptibility, and their detection is used in the diagnosis of a predisposition to these conditions.

[05] The invention also provides methods for the identification of compounds that modulate the expression of genes or the activity or the cellular organization of gene products involved in liver disease, as well as methods for the treatment of liver disease, which may involve the administration of such compounds to individuals exhibiting liver disease symptoms or tendencies.

BRIEF DESCRIPTION OF THE DRAWINGS

[06] Fig. 1: Protein expression of mutant K8 and K18 in explanted livers. (A): K8/18 immunoprecipitates were obtained from 1% Empigen solubilized normal liver or livers with keratin mutation. The immunoprecipitates were separated by isoelectic focusing followed by SDS-PAGE, then immunoblotting with anti-K8/K18 antibodies. Note that K8 and K18 in normal liver consists of two or three isoforms depending on their phosphorylation levels (a, b). In contrast, some of the mutant keratins contain four (K8) or five (K18) isoforms due to coexpression of the wild-type and mutant keratin with subsequent generation of altered charged species that have a slightly different mutation-induced isoelectric focusing point (d, f, g, h). (B): K8/18 immunoprecipitates were prepared from normal liver or liver with the K18 T102A mutation, then analyzed by SDS-PAGE. The K18 bands were cut out, digested with trypsin, then analyzed with a MALDI-TOF mass spectrometer. Note that a peak position at 818.3 was detected only in liver specimen with the K18 T102A mutation but not in normal liver. The mass difference of 30 between the wild-type and T102A K18 tryptic peptides (848.3 versus 818.3) corresponds to the HO-C-H species (two hydrogen, one oxygen and one carbon atoms with a mass of 30 daltons) that are present in threonine (the wild-type residue) but not in alanine (the mutant residue).

[07] Fig. 2: Keratin filament organization in human liver explants, and histologic findings of livers harboring the keratin mutations. (A): Human livers were sectioned, fixed in acetone and

double-stained with rabbit anti-K8/18 (red) or mouse anti-vimentin (green) antibodies. Inset in panel i shows control double staining using red and green fluorochrome-conjugated goat anti-rabbit and goat anti-mouse antibodies without adding any primary antibodies. All images were obtained using the same magnification. Bar in panel a = 20 μm. (B): Hematoxylin and eosin staining of explanted liver from two patients with acute fulminant hepatitis. Panel "a" is from a patient without a keratin mutation while panel "b" is from a patient with the K18 T102A mutation. The region outlined by a box in "b" is magnified in panel "c" to illustrate the cytoplasmic filamentous deposits noted primarily in livers of patients with keratin mutations.

[08] The above two figures demonstrate: (i) the presence of the keratin mutations at the protein level (Fig. 1) and (ii) although the immunofluorescence staining is not significantly altered in the livers with keratin mutation as compared to those with keratin mutation (Fig. 2A) there appears to be a unique histologic feature of cytoplasmic filamentous deposits that are observed primarily in livers of patients with keratin mutations.

DETAILED DESCRIPTION OF THE EMBODIMENTS

[09] Methods and compositions are provided for the diagnosis of a predisposition to liver or biliary tract disease, including, without limitation, viral hepatitis, hepatic artery thrombosis, biliary atresia, alcoholic cirrhosis and other acute or chronic toxic liver injury, cryptogenic cirrhosis, acute fulminant hepatitis, cystic fibrosis, primary biliary cirrhosis, diseases that are linked with cryptogenic cirrhosis, such as nonalcoholic steatohepatitis, and the like. The invention is based, in part, on the evaluation of the K8/K18 keratin genotype, for which alleles predisposing to disease are herein identified. This permits the definition of disease pathways and the identification of a target in the pathway that is useful diagnostically, in drug screening, and therapeutically.

[10] In one aspect of the present invention, methods are provided for determining a predisposition to liver disease in an individual. The methods comprise an analysis of genomic DNA in an individual for an allele of keratin K8 or K18 that confers an increased susceptibility to liver disease. Individuals are screened by analyzing their genomic K8 and/or K18 gene sequence for the presence of a predisposing allele, as compared to a normal sequence. Screening for the presence of the mutation can also be done using antibodies that specifically identify the keratin mutation.

[11] In addition to the provided sequence polymorphisms, the effect of a candidate polymorphism in a K8 or K18 sequence can be determined for association with a predisposition to liver disease. The candidate polymorphism may be analyzed, for example, for segregation

of the sequence polymorphism with the disease phenotype. A predisposing mutation will segregate with incidence of the disease. Alternatively, biochemical studies may be performed to determine whether a candidate polymorphism affects the quantity or quality (in terms of its distribution, interaction with binding partners, etc), or function of the protein.

[12] Intermediate filaments (IFs) are a structurally related family of cellular proteins that are intimately involved with the cytoskeleton. The common structural motif shared by all IFs is a central alpha-helical 'rod domain' flanked by variable N- and C-terminal domains. The rod domain, the canonical feature of IFs, has been highly conserved during evolution. The variable terminals, however, have allowed the known IFs to be classified into 6 distinct types by virtue of their differing amino acid sequences. Keratins compose types I and II. Type I and type II keratins are usually expressed as preferential pairs in equal proportions in cells, although filaments can be formed *in vitro* from heterologous IF subunits.

[13] Human keratin 18 is a type I IF protein subunit, whose expression is restricted in adults to a variety of so-called "simple-type" epithelial tissues. KRT18 is the most divergent of the type I keratins with N-terminal and C-terminal domains that are quite different from those of epidermal keratins. The KRT18 gene is 3,791 bp long and the keratin 18 protein is coded for by 7 exons. The genetic sequence of K18 may be found in Genbank, accession no. NM_000224. The exon structure of KRT18 has been conserved compared to that of other keratin genes, with the exception of a single 3-prime terminal exon that codes for the tail domain of the protein that is represented by 2 exons in epidermal keratins. Keratin 8 is a type II keratin, which is co-expressed with K18. The genetic sequence of K8 may be found in Genbank, accession no. NM_002273.

[14] Mutations in K8 that are associated with a predisposition to liver disease (all the amino acid numbers represent amino acids of the processed protein) include G52V (GGC→GTC); Y53H (TAT→CAT); G61C (GGC→TGC); R340H (CGT→CAT); G433S (GGC→AGC); R453C (CGC→TGC). Mutations in K18 that are involved with a predisposition to liver disease include T102A (ACC→GCC); H127L (CAT→CTT); R260Q (CGG→CAG); G339R (GGG→AGG) (see Table 3).

[15] Keratin K8 or K18 mutations that result in an amino acid substitution or deletion at any one of the mutated positions designated above may be generally defined to include K8 G52X; Y53X; G61X; R340X; G433X; R453X and K18 T102X; H127X; R260X; G339X, where X is any amino acid other than the naturally occurring amino acid as set forth in the published sequence of K8 or K18, and X may also refer to a deleted amino acid or amino acids. Mutations may also be specified in terms of the DNA sequence, and could include any deletions, or mutations in

the promoter or other regulatory regions that may affect RNA levels or stability under basal conditions or in response to any type of mechanical or nonmechanical stress that the liver may be exposed to due to internal or external factors.

[16] DNA encoding a K8/K18 protein may be cDNA or genomic DNA or a fragment thereof that encompasses one or more of the above identified polymorphisms. As known in the art, cDNA sequences have the arrangement of exons found in processed mRNA, forming a continuous open reading frame, while genomic sequences may have introns interrupting the open reading frame. The term K8/K18 gene shall be intended to mean the open reading frame encoding such specific polypeptides, as well as adjacent 5' and 3' non-coding nucleotide sequences involved in the regulation of expression, up to about 1 kb beyond the coding region, in either direction.

[17] The nucleic acid compositions of the subject invention encode all or a part of a K8 or K18 polypeptide comprising a polymorphism as described above. Fragments may be obtained of the DNA sequence by chemically synthesizing oligonucleotides in accordance with conventional methods, by restriction enzyme digestion, by PCR amplification, *etc.* For the most part, DNA fragments will be at least about 25 nt in length, usually at least about 30 nt, more usually at least about 50 nt. For use in amplification reactions, such as PCR, a pair of primers will be used. The exact composition of the primer sequences is not critical to the invention, but for most applications the primers will hybridize to the subject sequence under stringent conditions, as known in the art. It is preferable to chose a pair of primers that will generate an amplification product of at least about 50 nt, preferably at least about 100 nt. Algorithms for the selection of primer sequences are generally known, and are available in commercial software packages. Amplification primers hybridize to complementary strands of DNA, and will prime towards each other.

[18] The subject K8/K18 genes are isolated and obtained in substantial purity, generally as other than an intact mammalian chromosome. Usually, the DNA will be obtained substantially free of other nucleic acid sequences that do not include a K8/K18 sequence or fragment thereof, generally being at least about 50%, usually at least about 90% pure and are typically "recombinant", i.e. flanked by one or more nucleotides with which it is not normally associated on a naturally occurring chromosome. The subject nucleic acids may be used to identify expression of the gene in a biological specimen.

[19] A number of methods may be used for determining the presence of a predisposing mutation in an individual. Genomic DNA may be isolated from the individual or individuals that are to be tested. DNA can be isolated from any nucleated cellular source such as blood, hair

shafts, saliva, mucous, biopsy, feces, *etc.* Methods using PCR amplification can be performed on the DNA from a single cell, although it is convenient to use at least about 10^5 cells. Where large amounts of DNA are available, the genomic DNA is used directly. Alternatively, the region of interest is cloned into a suitable vector and grown in sufficient quantity for analysis, or amplified by conventional techniques. Of particular interest is the use of the polymerase chain reaction (PCR) to amplify the DNA that lies between two specific primers. The use of the polymerase chain reaction is described in Saiki *et al.* (1985) Science **239**:487, and a review of current techniques may be found in McPherson *et al.* (2000) PCR (Basics: From Background to Bench) Springer Verlag; ISBN: 0387916008. A detectable label may be included in the amplification reaction. Suitable labels include fluorochromes, *e.g.* fluorescein isothiocyanate (FITC), rhodamine, Texas Red, phycoerythrin, allophycocyanin, 6-carboxyfluorescein (6-FAM), 2',7'-dimethoxy-4',5'- dichloro-6-carboxyfluorescein (JOE), 6-carboxy-X-rhodamine (ROX), 6-carboxy-2',4',7',4,7-hexachlorofluorescein (HEX), 5-carboxyfluorescein (5-FAM) or N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA), radioactive labels, e.g. ^{32}P, ^{35}S, ^{3}H; *etc.* The label may be a two stage system, where the amplified DNA is conjugated to biotin, haptens, *etc.* having a high affinity binding partner, *e.g.* avidin, specific antibodies, *etc.*, where the binding partner is conjugated to a detectable label. The label may be conjugated to one or both of the primers. Alternatively, the pool of nucleotides used in the amplification is labeled, so as to incorporate the label into the amplification product.

[20] Primer pairs are selected from the K8/K18 genomic sequence using conventional criteria for selection. The primers in a pair will hybridize to opposite strands, and will collectively flank the region of interest. The primers will hybridize to the complementary sequence under stringent conditions, and will generally be at least about 16 nt in length, and may be 20, 25 or 30 nucleotides in length. The primers will be selected to amplify the specific region of the K8/K18 gene suspected of containing the predisposing mutation. Multiplex amplification may be performed in which several sets of primers are combined in the same reaction tube, in order to analyze multiple exons/introns/promoter and other regulatory regions simultaneously. Each primer may be conjugated to a different label.

[21] After amplification, the products may be size fractionated and evaluated for sequence polymorphisms. Fractionation may be performed by gel electrophoresis, particularly denaturing acrylamide or agarose gels. A convenient system uses denaturing polyacrylamide gels in combination with an automated DNA sequencer, see Hunkapillar et al. (1991) Science 254:59-74. The automated sequencer is particularly useful with multiplex amplification or pooled products of separate PCR reactions. Capillary electrophoresis may also be used for

fractionation. A review of capillary electrophoresis may be found in Landers, et al. (1993) BioTechniques 14:98-111. Hybridization with the variant sequence may also be used to determine its presence, by Southern blots, dot blots, *etc.* Single strand conformational polymorphism (SSCP) analysis, denaturing gradient gel electrophoresis (DGGE), and heteroduplex analysis in gel matrices is used to detect conformational changes created by DNA sequence variation as alterations in electrophoretic mobility or via HPLC type analysis (eg Wave System™). The hybridization pattern of a control and variant sequence to an array of oligonucleotide probes immobilised on a microarray, may also be used as a means of detecting the presence of variant sequences.

[22] The presence of a predisposing mutation is indicative that an individual is at increased risk of developing liver disease. The diagnosis of a disease predisposition allows the affected individual to seek early treatment, dietary measures, to avoid activities that increase risk for liver disease, and the like.

[23] In addition to genetic tests, the presence of the mutated polypeptide may be detected, by determination of the presence of polypeptide comprising the mutation using analytic methods such as mass spectrometry or immune-related methods such as mutant-specific antibodies, or by detecting the presence of cytoplasmic filamentous deposits.

[24] In a typical assay, a liver sample is assayed for the presence of K8 and/or K18 specific sequences by combining the sample with a K8 and/or K18 specific binding member, and detecting directly or indirectly the presence of the complex formed between the two members. The term "specific binding member" as used herein refers to a member of a specific binding pair, i.e. two molecules where one of the molecules through chemical or physical means specifically binds to the other molecule. In this particular case one of the molecules is K8 and/or K18, where K8 and/or K18 is any protein substantially similar to the amino acid sequence of the human polypeptide sequences of this family, as described above, or a epitope containing fragment thereof, and further comprising a predisposing mutation. The complementary members of a specific binding pair are sometimes referred to as a ligand and receptor. Testing can also be done using any source of genomic material from a given individual or any tissue that also expresses K8 and K18 (eg gastric, small or large intestinal biopsy).

[25] In the present specification and claims, the term "polypeptide fragments", or variants thereof, denotes both short peptides with a length of at least two amino acid residues and at most 10 amino acid residues, oligopeptides with a length of at least 11 amino acid residues, 20 amino acid residues, 50 amino acid residues, and up to about 100 amino acid residues; and

longer peptides of greater than 100 amino acid residues up to the complete length of the native polypeptide.

[26] Polypeptides detected by the present methods include naturally occurring alpha and beta subunits, as well as variants that are encoded by DNA sequences that are substantially homologous to one or more of the DNA sequences specifically recited herein, for example variants having at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 99.5% sequence identity. The specific binding pairs may include analogs, derivatives and fragments of the original specific binding member. For example, an antibody directed to a protein antigen may also recognize peptide fragments, chemically synthesized peptidomimetics, labeled protein, derivatized protein, etc. so long as an epitope is present.

[27] Immunological specific binding pairs include antigens and antigen specific antibodies or T cell antigen receptors. Recombinant DNA methods or peptide synthesis may be used to produce chimeric, truncated, or single chain analogs of either member of the binding pair, where chimeric proteins may provide mixture(s) or fragment(s) thereof, or a mixture of an antibody and other specific binding members. Antibodies and T cell receptors may be monoclonal or polyclonal, and may be produced by transgenic animals, immunized animals, immortalized human or animal B-cells, cells transfected with DNA vectors encoding the antibody or T cell receptor, etc. The details of the preparation of antibodies and their suitability for use as specific binding members are well-known to those skilled in the art.

[28] Alternatively, monoclonal or polyclonal antibodies are raised to K8 and/or K18 polypeptides comprising a predisposing mutation. The antibodies may be produced in accordance with conventional ways, immunization of a mammalian host, e.g. mouse, rat, guinea pig, cat, rabbit, dog, etc., fusion of resulting splenocytes with a fusion partner for immortalization and screening for antibodies having the desired affinity to provide monoclonal antibodies having a particular specificity. These antibodies can be used for affinity chromatography, ELISA, RIA, and the like. The antibodies may be labeled with radioisotopes, enzymes, fluorescers, chemiluminescers, or other label, which will allow for detection of complex formation between the labeled antibody and its complementary epitope. Generally the amount of bound K8 and/or K18 detected will be compared to negative control samples from normal tissue or cells.

[29] Screening assays identify compounds that modulate the expression or structure of K8/K18. Such compounds may include, but are not limited to peptides, antibodies, or small

organic or inorganic compounds. Methods for the identification of such compounds are described below.

[30] Cell- and animal-based systems can act as models for liver disease and are useful in such drug screening. The animal- and cell-based models may be used to identify drugs, pharmaceuticals, therapies and interventions that are effective in treating liver disease. In addition, such animal models may be used to determine the LD_{50} and the ED_{50} in animal subjects, and such data can be used to determine the *in vivo* efficacy of potential liver disease treatments. Animal-based model systems of liver disease may include, but are not limited to, non-recombinant and engineered transgenic animals. Animal models exhibiting liver disease symptoms may be engineered by utilizing, for example, K8 and/or K18 gene sequences in conjunction with techniques for producing transgenic animals that are well known to those of skill in the art. For example, target gene sequences may be introduced into, and knocked out or overexpressed in the genome of the animal of interest. Animals of any species, including, but not limited to, mice, rats, rabbits, guinea pigs, pigs, micro-pigs, goats, and non-human primates, *e.g.*, baboons, monkeys, and chimpanzees may be used to generate liver disease animal models.

[31] Any technique known in the art may be used to introduce a target gene transgene into animals to produce the founder lines of transgenic animals. Such techniques include, but are not limited to pronuclear microinjection (Hoppe, P. C. and Wagner, T. E., 1989, U.S. Pat. No. 4,873,191); retrovirus mediated gene transfer into germ lines (Van der Putten et al., 1985, Proc. Natl. Acad. Sci., USA 82:6148-6152); gene targeting in embryonic stem cells (Thompson et al., 1989, Cell 56:313-321); electroporation of embryos (Lo, 1983, Mol Cell. Biol. 3:1803-1814); and sperm-mediated gene transfer (Lavitrano et al., 1989, Cell 57:717-723); *etc.*

[32] Specific cell types within the animals may be analyzed and assayed for cellular phenotypes characteristic of liver disease. Further, such cellular phenotypes may include a particular cell type's fingerprint pattern of expression as compared to known fingerprint expression profiles of the particular cell type in animals exhibiting liver disease symptoms.

[33] Cells that contain and express K8/K18 can be utilized to identify compounds that exhibit pharmacologic activity of interest, in the prevention of liver disease. Cells of a cell type known to be involved in liver disease may be transfected with sequences capable of increasing or decreasing the amount of K8 and/or K18 gene expression within the cell. For example, K8/K18 gene sequences may be introduced into, and overexpressed in, the genome of the cell of interest, or, if endogenous target gene sequences are present, they may be either

overexpressed or, alternatively disrupted in order to underexpress or inactivate target gene expression.

[34] Transfection of target gene sequence nucleic acid may be accomplished by utilizing standard techniques. Transfected cells can be evaluated for the presence of the recombinant K8/K18 gene sequences, for expression and accumulation of K8/K18 gene mRNA, and for the presence of recombinant K8/K18 protein. Where a decrease in K8/K18 gene expression is desired, standard techniques may be used to demonstrate whether a decrease in expression is achieved.

[35] *In vitro* systems may be designed to identify compounds capable of preventing or treating liver disease. Such compounds may include, but are not limited to, peptides made of D-and/or L-configuration amino acids, phosphopeptides, antibodies, and small organic or inorganic molecules. For example, assays may be used to identify compounds that improve liver function involves preparing a reaction mixture of K8/K18 and a test compound under conditions and for a time sufficient to allow the two components to interact, and detecting the resulting change in the polypeptide structure. Alternatively, a simple binding assay can be used as an initial screening method. These assays can be conducted in a variety of ways. For example, one method to conduct such an assay would involve anchoring K8/K18 protein or a test substance onto a solid phase and detecting complexes anchored on the solid phase at the end of the reaction. In another embodiment of such a method, the assay tests the presence of products modulated by K8/K18.

[36] In a binding assay, the reaction can be performed on a solid phase or in liquid phase. In a solid phase assay, the nonimmobilized component is added to the coated surface containing the anchored component. After the reaction is complete, unreacted components are removed under conditions such that any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the previously nonimmobilized component is pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the previously nonimmobilized component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the previously nonimmobilized component (the antibody, in turn, may be directly labeled or indirectly labeled with a labeled anti-Ig antibody).

[37] Alternatively, a binding reaction can be conducted in a liquid phase, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for target gene product or the test compound to anchor any

complexes formed in solution, and a labeled antibody specific for the other component of the possible complex to detect anchored complexes.

[38] Cell-based systems such as those described above may be used to identify compounds that act to ameliorate liver disease symptoms. For example, such cell systems may be exposed to a test compound at a sufficient concentration and for a time sufficient to elicit such an amelioration of liver disease symptoms in the exposed cells. After exposure, the cells are examined to determine whether one or more of the liver disease cellular phenotypes has been altered to resemble a more normal or more wild type, non-liver disease phenotype.

[39] In addition, animal-based disease systems, such as those described, above may be used to identify compounds capable of ameliorating disease symptoms. Such animal models may be used as test substrates for the identification of drugs, pharmaceuticals, therapies, and interventions, which may be effective in treating disease. For example, animal models may be exposed to a compound, suspected of exhibiting an ability to ameliorate liver disease symptoms, at a sufficient concentration and for a time sufficient to elicit such an amelioration of disease symptoms in the exposed animals. The response of the animals to the exposure may be monitored by assessing the reversal of disorders associated with disease.

[40] With regard to intervention, any treatments that reverse any aspect of liver disease symptoms may be considered as candidates for human disease therapeutic intervention. Dosages of test agents may be determined by deriving dose-response curves.

[41] Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD_{50} /ED_{50}. Compounds that exhibit large therapeutic indices are preferred. While compounds that exhibit toxic side effects may be used, care should be taken to design a delivery system that targets such compounds to the site of affected tissue in order to minimize potential damage to uninfected cells and, thereby, reduce side effects.

[42] The data obtained from the cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose

may be formulated in animal models to achieve a circulating plasma concentration range that includes the IC_{50} (i.e., the concentration of the test compound which achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography.

[43] Pharmaceutical compositions for use in accordance with the present invention may be formulated in conventional manner using one or more physiologically acceptable carriers or excipients. Thus, the compounds and their physiologically acceptable salts and solvates may be formulated for administration by oral, buccal, parenteral or rectal administration.

[44] For oral administration, the pharmaceutical compositions may take the form of, for example, tablets or capsules prepared by conventional means with pharmaceutically acceptable excipients such as binding agents (e.g., pregelatinised maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose); fillers (e.g., lactose, microcrystalline cellulose or calcium hydrogen phosphate); lubricants (e.g., magnesium stearate, talc or silica); disintegrants (e.g., potato starch or sodium starch glycolate); or wetting agents (e.g., sodium lauryl sulphate). The tablets may be coated by methods well known in the art. Liquid preparations for oral administration may take the form of, for example, solutions, syrups or suspensions, or they may be presented as a dry product for constitution with water or other suitable vehicle before use. Such liquid preparations may be prepared by conventional means with pharmaceutically acceptable additives such as suspending agents (e.g., sorbitol syrup, cellulose derivatives or hydrogenated edible fats); emulsifying agents (e.g., lecithin or acacia); non-aqueous vehicles (e.g., almond oil, oily esters, ethyl alcohol or fractionated vegetable oils); and preservatives (e.g., methyl or propyl-p-hydroxybenzoates or sorbic acid). The preparations may also contain buffer salts, flavoring, coloring and sweetening agents as appropriate. Preparations for oral administration may be suitably formulated to give controlled release of the active compound. For buccal administration the compositions may take the form of tablets or lozenges formulated in conventional manner.

[45] The compounds may be formulated for parenteral administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampoules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

[46] In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

[47] The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may for example comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration.

[48] The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one specific K8/K18 nucleic acid reagent described herein, which may be conveniently used, e.g., in clinical settings, for prognosis of patients susceptible to liver disease.

[49] Before the subject invention is described further, it is to be understood that the invention is not limited to the particular embodiments of the invention described below, as variations of the particular embodiments may be made and still fall within the scope of the appended claims. It is also to be understood that the terminology employed is for the purpose of describing particular embodiments, and is not intended to be limiting. Instead, the scope of the present invention will be established by the appended claims.

[50] In this specification and the appended claims, the singular forms "a," "an" and "the" include plural reference unless the context clearly dictates otherwise. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs.

[51] Where a range of values is provided, it is understood that each intervening value, to the tenth of the unit of the lower limit unless the context clearly dictates otherwise, between the upper and lower limit of that range, and any other stated or intervening value in that stated range, is encompassed within the invention. The upper and lower limits of these smaller ranges may independently be included in the smaller ranges, and are also encompassed within the invention, subject to any specifically excluded limit in the stated range. Where the stated range includes one or both of the limits, ranges excluding either or both of those included limits are also included in the invention.

[52] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs. Although any methods, devices and materials similar or equivalent to those described herein can be used in the practice or testing of the invention, the preferred methods, devices and materials are now described.

[53] All publications mentioned herein are incorporated herein by reference for the purpose of describing and disclosing the subject components of the invention that are described in the publications, which components might be used in connection with the presently described invention.

EXPERIMENTAL

Methods

[54] *Patients:* We included for the analysis specimens of 467 explanted livers that were obtained from the liver transplantation units at Stanford University, the University of California San Francisco, and California Pacific Medical Center. Peripheral blood samples from 349 healthy volunteers were obtained from the Stanford Blood Bank and used for genomic DNA isolation. In addition and when available, blood samples were obtained from patients with the identified keratin mutations and/or from their children. Of the 467 liver samples, 153 were previously analyzed and the remaining 314 liver explants are newly described and were used for genomic DNA isolation, immunofluorescence staining and other biochemical tests. The patients' sex and racial/ethnic background were determined from patients' medical records. No information could be found on 15 patients due to lack of records or to retransplant. For the control samples, anonymous information regarding sex and race was provided by the Stanford Blood Bank. The diagnoses were based on the United Network for Organ Sharing transplant listing. Medical records of all patients with a keratin mutation were reviewed and the diagnosis was confirmed.

[55] *Histopathology and statistical analysis:* Pathology slides from the explanted livers with keratin mutations, and matched liver disease controls, were reviewed by a single pathologist who did not know which specimens harbored the keratin mutations. Slides from the explanted livers of all 17 patients with keratin mutations, as well as disease-matched controls, were examined and scored for the presence or absence of features including Mallory and acidophil bodies, cell size, ground glass cytoplasm, and dysplasia. Images of the hematoxylin and eosin stained liver sections were obtained using a Nikon Eclipse E1000 microscope with a 40x

objective. Data analysis was conducted using the Fisher's exact test performed with Statistical Analyzing System software (SAS).

[56] *Molecular methods:* Genomic DNA was prepared using a Dneasy tissue kit (QIAGEN Inc., Chatsworth, CA). Exonic regions were amplified using previously described primers corresponding to amino acids: 67-131, 225-273, and 322-389 (for K18) and 50-107 and 341-401 (for K8) (Ku *et al.* (2001) *N. Engl. J. Med.* **344**, 1580-1587). Regions chosen for amplification included the epidermal keratin domains where most of the mutations have been identified (Irvine & McLean (1999) *Br. J. Dermatol.* **140**, 815-828). The polymerase chain reaction amplified products were analyzed using Mutation Detection Enhancement gels (FMC Bioproducts, Rockland, ME), and any samples with a "shift" pattern suggestive of a mutation were sequenced in the forward and reverse directions to confirm the presence of a mutation. Alternatively, samples are analyzed for mutation using the Wave System™ (Transgenomic Inc, San Jose, CA).

[57] *Biochemical methods*: Tissues were homogenized in phosphate buffered saline containing 1% n-dodecyl-*N*,*N*-dimethylglycine (Empigen BB, Calbiochem-Novabiochem, San Diego, CA), 5 mM EDTA, and protease inhibitors. Homogenized samples were solubilized for 30 minutes, pelleted then used for immunoprecipitation of K8/K18. Precipitates were analyzed by: (i) SDS polyacrylamide gel electrophoresis (PAGE), under reducing or non-reducing conditions, then Coomassie staining, (ii) SDS-PAGE then immunoblotting, or (iii) two-dimensional gels using isoelectric focusing (horizontal direction) and SDS-PAGE (vertical direction) then immunoblotting.

[58] *Mass spectrometry analysis:* Separated K8 and K18 bands were cut out from preparative gels, reduced with dithiothreitol, alkylated with iodoacetamide, and then digested with trypsin in 50 mM ammonium bicarbonate (pH 7.8) using a standard in-gel-digestion procedure. Extracted K8 or K18 tryptic peptides were desalted using a C18 ZipTip (Millipore, MA) then eluted with 50% acetonitrile-0.1% trifluoroacetic acid (TFA). A 1 µl aliquot of the eluant was mixed with equal volume of matrix solution (saturated a-cyano-4-hydroxycinnamic acid in 0.1% TFA-50% acetonitrile in water) and analyzed by a MALDI-TOF mass spectrometer (Bruker Biflex III) equipped with a nitrogen 337 nm laser. The mass spectra were acquired in the reflectron mode. Internal mass calibration was performed with two trypsin autodigested fragments (842.5 and 2211.1 Da). K8 tryptic peptides were also digested with CNBr and similarly analyzed.

[59] *Immunofluorescence staining:* Snap-frozen liver explants were embedded in optimum cutting temperature compound, sectioned then fixed in acetone (-20 °C, 10 min). Sections were

double stained with antibodies directed to K8/K18 (13) or vimentin (NeoMarkers, Freemont, CA). Flourescence images were obtained using an MRC 1024ES confocal scanner (BioRad, Hercules, CA) coupled to a Nikon Eclipse TE300 microscope.

[60] *Identification of K8 and K18 mutations:* We tested DNA extracted from liver explants or peripheral blood for the presence of K8 or K18 mutations. Two cohorts were examined, whose demographics are summarized in Table 1: a group of 467 patients with a variety of liver diseases, and a control group of 349 blood bank donors. The ethnic background of the two cohorts was generally similar except for a higher preponderance of Caucasian patients in the control group.

Table 1.

Racial/Ethnic Background and Sex of Patients and Controls

Characteristics	Liver Disease Patients		Blood Bank Controls	
White	274	58.6%	268	77%
Male	139		154	
Female	135		114	
Black	26	5.6%	9	3%
Male	9		5	
Female	17		4	
Hispanic	67	14.3%	42	12%
Male	28		21	
Female	39		21	
Asian/Pacific Islander	57	12.1%	23	7%
Male	36		12	
Female	21		11	
Middle Eastern/Indian	20	4.2%	6	2%
Male	14		2	
Female	6		4	
Native American	2	0.8%	1	0.30%
Male	1		0	
Female	1		1	
Unknown	21	4.4%	0	0%
Total	467		349	

[61] The etiology of the liver diseases is broad (Table 2), most of which is noncryptogenic (based on clinical criteria, 68 of the 467 patients were classified as having cryptogenic liver disease; Table 2). We included the control blood bank cohort in order to address which mutations identified in the liver disease cohort are likely to represent "true" mutations versus polymorphisms found in the general population. Forty nine of the 467 liver disease patients had K8 or K18 heterozygous missense point mutations that were confirmed by DNA sequencing, which resulted in amino acid substitutions (Table 3).

Table 2. Liver Disease Etiologies and Frequency of Keratin Mutations

Etiology of Liver Disease	# of Patients (# with keratin mutations)	% Keratin Mutations
Hepatitis C	80 (8)	10.0
Hepatitis C/Alcohol	28 (4)	14.2
Hepatitis B	44 (3)	6.8
Biliary Atresia	47 (3)	6.4
Alcohol	33 (3)	9.1
Cryptogenic	68 (7)	10.3
Primary Biliary Cirrhosis	12 (2)†	16.7
Primary Sclerosing Cholangitis	15 (1)	6.7
Acute Fulminant Hepatitis	35 (4)†	11.4
Neonatal Hepatitis	9 (2)	22.2
Autoimmune Hepatitis	33 (2)	6.1
Metabolic/Genetic*	23	8.7
Cystic Fibrosis	(1)	
Metabolic/other	(1)	
Primary Liver Cancer**	5 (0)	
Drug induced Liver Failure	9 (1)	11.1
Other§	26 (7)	26.9
Total	467 (49)	10.5

* Metabolic/genetic diagnoses included 4 Wilson's disease, 3 hemochromatosis, 3 α1-antitrypsin deficiency, 2 cystic fibrosis, 3 primary oxalosis, 1 Crigler-Najjar, 1 ornithine transcarbamoylase deficiency, 1 Nieman-Pick, 1 arginosuccinicaciduria, 1 tyrosinemia, 1 cirtrolemia, 1 glycogen storage, and 1 "metabolic disease" that is unclassified.

** Patients with viral hepatitis and hepatoma were included under the appropriate viral hepatitis category. Primary liver cancers included 1 hepatoma, 3 hemangio-endotheliomas, and 1 hepatosarcoma.

† One patient with primary biliary cirrhosis had a double mutant (K8 R340H and K18 R260Q), and one patient with acute fulminant hepatitis also had a double mutant (K8 R340H and K18 T102A). All other patient had a single mutation.

§ The "Other" category of liver diseases included Budd-Chiari, hepatic artery thrombosis, polycystic disease, Caroli's disease, Byler's disease, 2 chronic rejection, primary graft nonfunction, Klatskin tumor, parenteral nutrition-induced, carcinoid, hepatitis B and C, hepatitis B and alcohol, multiple adenomas, secondary biliary cirrhosis, veno-occlusive disease, and congenital hepatic fibrosis. At least 11 of the patients screened had received a prior orthotopic liver transplant. For a few patients, their disease etiology could not be discerned from the medical records.

Table 3. K8/K18 Mutations in Human Liver Diseases

	Mutations	# of mutation carriers from

	Amino Acid	Nucleotide	Liver disease cohort (467)	Blood bank controls (349)
K8	**G52V**	**GGC→GTC**	**1**	**None**
	Y53H	**TAT→CAT**	**5**	**1**
	G61C	**GGC→TGC**	**6**	**1**
	R340H	**CGT→CAT**	**29**	**9**
	G433S	**GGC→AGC**	**4**	**1**
	R453C	**CGC→TGC**	**1**	**None**
	I62V*	ATC→GTC	1	7
	L71L**	CTG→CTA	1	None
	A318S*	GCT→TCT	5	2
	R301C*	CGC→TGC	None	1
	E376E**	GAG→GAA	2	-
	V460M*	GTG→ATG	None	1
	V479I*	GTC→ATC	None	2
K18	**T102A**	**ACC→GCC**	**1**	**None**
	H127L	**CAT→CTT**	**2**	**None**
	R260Q	**CGG→CAG**	**1**	**None**
	G339R	**GGG→AGG**	**1**	**None**
	S229T*	AGC→ACC	2	4
	Y330Y**	TAC→TAT	1	None
K8			46/467	2/349
K18			5/467	None
K8/18			**49†/467**	**12/349**

Single letter standard abbreviations are used to represent amino acids and nucleotides. Sequences with bold letter refer to mutations that pose a potential risk factor for subsequent development of cirrhosis, based on analysis of the liver disease cohort and the blood bank control group. Single asterisks (*) highlight amino acid substitutions (e.g. K8 I62V and K18 S229T) that are considered polymorphisms since they were found at similar, or higher, incidence in the control cohort as compared with the liver disease group. All the patients with the K8 A318S mutation also had a K8 R340H mutation. Double asterisks (**) highlight likely "silent" nucleotide mutations that do not result in any amino acid change. The total number of K8/K18 mutations shown represents true mutations and does not include "silent" mutations or polymorphisims.

† Two patients had a double mutant (K8 R340H and K18 R260Q, or K8 R340H and K18 T102A). All other patient had a single mutation.

Table 4. Diseases and Ethnicities Associated with Different Keratin Mutations in Liver Patients and Controls

	Liver Disease Patients		Blood Bank Controls
Keratin Mutation§	**Liver Disease**	**No. with mutation/Ethnicity***	**No. with mutation/Ethnicity**
K8 G52V	Viral Hepatitis	1/White	none/-
K8 Y53H	Viral Hepatitis, BA, CC	5/3 Black, 1 White, 1 Hispanic	1/Black

K8 G61C	Viral Hepatitis,Alcohol,CC,CF	6/1 Black, 4 White, 1 Unknown	1/White
K8 R340H	Viral Hepatitis, AFH, others	29/14 White, 10 Hispanic, 1 Indian, 4 Unknown	9/8 White, 1 Hispanic
K8 G433S	Viral Hepatitis, Alcohol, BA	4/2 Black, 2 Unknown	1/Black
K8 R453C	CC	1/Unknown	none/-
K18 T102A	AFH	1/Hispanic	none/-
K18 H127L	Metabolic, CC	2/White	none/-
K18 R260Q	PBC	1/Hispanic	none/-
K18 G339R	Hepatic Artery Thrombosis	1/Unknown	none/-
Prevalence of Keratin Mutations		49**/467 (10.5%)†	12/349 (3.4%)†

BA= Biliary Atresia, CC= Cryptogenic Cirrhosis, CF= Cystic Fibrosis, PBC= Primary Biliary Cirrhosis, AFH= Acute Fulminant Hepatiti

11 Hispanic (7 female/4 male), 1 Indian (1 female) and 9 unknown.

[62] Also, "silent" point mutations that did not result in any amino acid substitutions (K8 L71L/E376E; K18 Y330Y) were identified in the liver disease cohort but not in the control group (Table 3).

[63] The mutations that were identified in 49 of 467 patients represent a mutation frequency of 10.5%, as compared with a mutation frequency of 3.4% found in 12 of 349 controls (P=0.0001; Tables 3 and 4). Given the demographics of patients with keratin mutations, there does not appear to be any obvious accumulation of keratin mutations in a particular sex or ethnic background (Table 4). Since most of the specimen that we analyzed consisted of liver explants, we also tested blood specimen for the germline presence and transmission of the identified keratin mutations, in order to exclude the possibility that the mutations we identified occurred during development of disease. Of the 49 independent patients with K8/K18 mutations we were able to locate 4 patients and/or their offspring. All four of these patients and/or their offspring blood specimen had the identical heterozygous keratin mutation to that identified in the diseased explanted liver (Table 5). Therefore, the K8/K18 mutations we identified are not a consequence of the liver disease but, rather, predispose their carriers to subsequent development of liver disease.

[64] *Expression of mutant keratin proteins:* We examined, biochemically, the liver explant specimens from some of the mutation carriers within the cohort of 467 patients in order to

confirm the presence of the mutation at the protein level. Mutations that were examined included 7 types: K8 G52V/Y53H/G61C and K18 T102A/H127L/R260Q/G339R (Table 3). The presence of the K8 G61C protein was confirmed as we did previously (Ku et al, New England Journal of Medicine 344:1580-1587, 2001), by formation of K8 dimers (under nonreducing gel conditions) due to the newly introduced cysteine (normally absent in K8/K18). We also used two-dimensional gels to separate proteins based on their charge, and thereby confirmed the presence of the K8 Y53H and K18 H127L/R260Q/G339R species (Fig.1A). These four K8/K18 mutations generated proteins with a different charge as compared to their wild-type counterparts, and resulted in new isoforms (4 isoforms instead of 2 for mutant K8, and 5 isoforms instead of 3 for mutant K18, Fig.1A).

[65] Two-dimensional gel analysis was, however, not informative for mutations that do not significantly alter the isoelectric point (Fig.1A, K8 G52V and K18 T102A variants). For these mutations, we compared the mass spectrometric profiles of protease-generated fragments of wildtype and mutant keratins and tested for the presence of peptides that have a mutation-altered mass. As shown in Fig.1B, presence of the K18 T102A protein was confirmed by detection of its alanine-102-containing peptide with a predicted mass of 818.3 (in addition to the wild-type threonine-102-containing peptide with a predicted mass of 848.3). A similar analysis was attempted for K8 G52V but no peptide that corresponds to a valine-to-glycine substitution was detected, likely due to inability to recover it from the isolation column.

[66] *Effect of keratin mutations on keratin filament organization and liver histology:* We compared keratin filament organization in liver explants of patients with and without keratin mutations. We did not observe any generalized keratin mutation-specific organization defects as tested by immunofluorescence staining (Fig. 2A). The diseased livers (with or without keratin mutations) had reorganization of the keratins filaments with the most prominent feature being thickening and partial collapse (Fig. 2A, panels d and g) as compared with normal liver keratin staining (Fig. 2A, panel a). The diseased livers had variable but significant vimentin-positive staining (Fig. 2A, panels e, h), which was used as a fibroblast/stellate cell marker, as compared with normal liver (Fig. 2A, panel b). Vimentin staining did not correlate with the presence of keratin mutations, and did not involve hepatocytes (Fig. 2A; merged images c, f, i). Analysis of additional liver samples with proper attention to sample handling will be needed to better assess any potential keratin mutation-induced effects on keratin organization.

[67] We also asked if any histologic features identified by light microscopy could distinguish cirrhotic livers of patients with and without keratin mutations. Features such as Mallory's hyaline, acidophil bodies, enlarged hepatocytes, ground glass cytoplasm and dysplasia were

found in keratin-mutant and non-keratin-mutant livers. However, close inspection of the liver specimen(s) showed a unique accumulation in some hepatocytes of cytoplasmic filamentous arrays (Fig. 2B). When coding of the slides (with mutant or nonmutant keratin) was opened, the findings indicated that the filamentous deposits were found in 10 of 17 tested patients with keratin mutations but in only 3 of 16 disease-matched controls (p=0.03). When patients with only primary hepatocellular diseases (cryptogenic, viral hepatitis, alcohol, acute fulminant hepatitis) were included in the analysis, 10 of 11 explants with a keratin mutation contained the cytoplasmic filamentous deposits as compared with 3 of 13 disease-matched controls (p=0.001). The nature of the filamentous deposits remains to be determined, but they do not appear to correspond to aggregated keratins since they were not recognized by anti-keratin antibodies (which may reflect epitope masking.

[68] Mutations in keratins and other IF family members, including lamins, desmin, glial fibrillary acidic protein (GFAP) and neurofilaments, are well-established causes of a wide range of tissue specific human diseases. The list of newly identified diseases associated with IF proteins continues to grow, including the latest association of K8 with cryptogenic cirrhosis, GFAP with Alexander disease and the neurofilament-L chain with Charcot-Marie-Tooth type-2. One distinguishing feature of K8/K18 mutations, as compared with epidermal keratin mutations involving K5/K14/K1/K10, is that the epidermal keratin diseases are typically autosomal dominant with ~100% penetrance. In contrast, K8/K18 mutations appear to be risk factors with variable penetrance, rather than direct causes of disease. In support of this, the location of the characterized K8/K18 mutations does not involve conserved pan-keratin domain mutation hot spots that have been identified in epidermal keratins. Apparent absence of such mutations suggests that they may be lethal, given that K8/K18 are among the earliest expressed keratins during embryogenesis. Also, three independent patients with K8 G61C, K18 H127L, or K18 R260Q mutations had germline transmission of the mutations to their children (Table 5).

Table 5. Germline Presence and Transmission of K8/K18 Mutations

Keratin mutation	Liver disease	Mutation in blood of	
		patients	offspring
K8 Y53H	Hepatitis B	Yes	N.A.
K8 G61C	Cryptogenic	Yes	Yes (in 3 of 4 tested)
K18 H127L	Cryptogenic	N.A.	Yes (1 tested)
K18 R260Q	PBC	Yes	Yes (1 tested)

N.A.= not available

[69] The ages of the offspring with the keratin mutations range from 31-52, but none of these carriers have apparent liver disease, based on clinical history and serologic testing. These observations support a "multi-hit" hypothesis, whereby one major "hit" is carrying a relevant K8/K18 mutation with subsequent "hits" including underlying liver disease or exposure to injurious factors such as toxins or viruses. Clinical and natural history studies can be used to define the relative risk of subsequent development of liver disease, or the relative increase in progression of an underlying liver disease, in those who carry specific K8/K18 mutations.

[70] The significant number of patients described in this study, with new and previously described K8/K18 mutations, provide several insights into keratin-associated liver diseases. For example, only one K18 H127L mutation was previously described in a patient with cryptogenic cirrhosis, but the results herein corroborate this mutation in a different liver disease patient and add several other new K18 mutation sites (Table 3). It appears that K18 H127L, K8 Y53H/G61C/G433S, and most prominently K8 R340H are emerging as mutation hot spots. These mutations were found in 2, 5, 6, 4 and 29 of the 49 patients with K8/K18 mutations, respectively (Table 3), and collectively make up ~94% of the K8/K18 mutations identified to date, while the K8 R340H mutation alone makes up ~59% of all K8/K18 mutations identified to date. Analysis of additional liver disease patients will help determine if these mutation hot spots maintain their frequency. Also, search for additional keratin mutation carriers in a broad range of cryptogenic and noncryptogenic liver diseases is clearly warranted.

[71] When we initially identified K8 and K18 mutations in 6 patients, all 6 had cryptogenic liver disease. This liver disease makes up nearly 10% of all patients who undergo liver transplantation. In this cryptogenic liver disease cohort 7 of 68 patients (10.3%) have K8 or K18 mutations. However and more importantly, our more significant findings are that keratin mutations are also just as common (10.5%) in the noncryptogeic liver disease group (Table 2) that accounts for the remaining 90% of liver transplantations (based on the patient groups we studied). The association of keratin mutations with cryptogenic liver disease raises the possibility that some diseases that are linked with this type of cirrhosis, such as nonalcoholic steatohepatitis, may also be associated with keratin mutations. This potential association is supported recent work done in animal models that we have recently submitted for publication (Tao et al, submitted). More K8 and/or K18 mutations may be identified as we are in the process of completing the characterization of the entire coding and promoter regions (nearly 80% of K8 and 40% of K18 coding regions have been completed).

[72] Although the mechanisms by which keratin mutations predispose to cirrhosis remain to be defined, already known and emerging keratin functions are likely to be involved. For example, multiple transgenic mouse model studies showed that K8/K18 serve the essential function of protecting hepatocytes from a variety of stresses including agents that cause acute (e.g. acetaminophen) or chronic (e.g. griseofulvin) injury, and agents that induce apoptosis (e.g. Fas antibody). K8/K18 may also be involved in protein targeting to the apical compartment of polarized epithelia, interacting with apoptotic machinery proteins, cell signaling and regulating the availability of abundant cellular proteins. Hence, keratin mutations may potentially act at a number of functional cellular nodes. One surrogate marker of keratin function is cytoplasmic filament organization, which was shown to be abnormally altered, only after stress exposure, in the K8 Y53H/G61C mutations. Our observation of preferential cytoplasmic filamentous deposits in cirrhotic livers of patients with keratin mutations is likely to be relevant and is reminiscent of Rosenthal fibers that are seen in association with Alexander Disease. The nature and pathogenesis of these deposits and their association with keratin-related liver disease remain to be investigated, but they are morphologically distinct from Mallory body-type deposits.

[73] It is evident that subject invention provides a convenient and effective way of determining whether a patient will be susceptible to liver disease. The subject methods will provide a number of benefits, including preventive treatment and diet. As such, the subject invention represents a significant contribution to the art.

WHAT IS CLAIMED IS:

1. A method for detecting a predisposition to liver disease in an individual, the method comprising:

analyzing an individual for quantitative or qualitative change in phenotype or genotype of keratin K8 or K18.

2. The method of Claim 1, wherein said liver disease is a noncryptogenic liver disease.

3. The method of Claim 2, wherein said human keratin genotype is one or more of K8 G52X; Y53X; G61X; R340X; G433X; R453X and K18 T102X; H127X; R260X; G339X, where X is any amino acid other than the naturally occurring amino acid or a deleted amino acid. The mutant genotype may also involve other mutation sites that involve the coding or noncoding regions of the K8 or K18 genes.

4. The method of Claim 3, wherein said analyzing the genomic sequence comprises the steps of:

amplifying a region of the K8 or K18 coding or noncoding sequences from isolated genomic DNA to provide an amplified fragment;

detecting the presence of a polymorphic sequence in said amplified fragment.

5. The method of Claim 4, wherein said detecting step comprises hybridization with a probe specific for the sequence of said polymorphism.

6. The method of Claim 3, wherein said detecting step comprising contacting a cell, tissue or potentially a serum sample with an antibody specific for one or more of said polymorphisms.

7. A method of screening for biologically active agents that affect susceptibility to liver disease, the method comprising:

combining a candidate biologically active agent with any one of:

(a) a K8/K18 polypeptide comprising one or more of K8. G52X; Y53X; G61X; R340X; G433X; R453X and K18 T102X; H127X; R260X; G339X, where X is any amino acid other than the naturally occurring amino acid or a deleted amino acid;

(b) a cell comprising a nucleic acid encoding a K8/K18 polypeptide comprising one or more of K8 G52X; Y53X; G61X; R340X; G433X; R453X and K18 T102X; H127X; R260X; G339X, where X is any amino acid other than the naturally occurring amino acid or a deleted amino acid; or a cell expressing another K8 or K18 mutant that alters K8/K18 filament organization such as the K18 R89C which causes keratin filament collapse; or

(c) a non-human transgenic animal model for liver disease comprising an exogenous and stably transmitted gene encoding a K8/K18 polypeptide comprising one or more of K8 G52X; Y53X; G61X; R340X; G433X; R453X and K18 T102X; H127X; R260X; G339X, where X is any amino acid other than the naturally occurring amino acid or a deleted amino acid; or a transgenic animal model expressing another K8 or K18 mutant that alters K8/K18 filament organization such as the K18 R89C which causes keratin filament collapse and

determining the effect of said agent susceptibility to liver disease.

ABSTRACT OF THE INVENTION

[74] Keratin 8 and 18 (K8/K18) mutations are shown to be associated with a predisposition to liver or biliary tract disease, particularly noncryptogenic liver disease. Unique K8/K18 mutations are shown in patients with diseases including but without limitation to viral hepatitis, hepatic artery thrombosis, biliary atresia, alcoholic cirrhosis and other acute or chronic toxic liver injury, cryptogenic cirrhosis, acute fulminant hepatitis, cystic fibrosis, primary biliary cirrhosis, diseases that are linked with cryptogenic cirrhosis, such as nonalcoholic steatohepatitis, and the like. Livers with keratin mutations had increased incidence of cytoplasmic filamentous deposits. Therefore, K8/K18 are susceptibility genes for developing cryptogenic and noncryptogenic forms of liver disease. Alleles are associated with disease susceptibility, and their detection is used in the diagnosis of a predisposition to these conditions.

A.

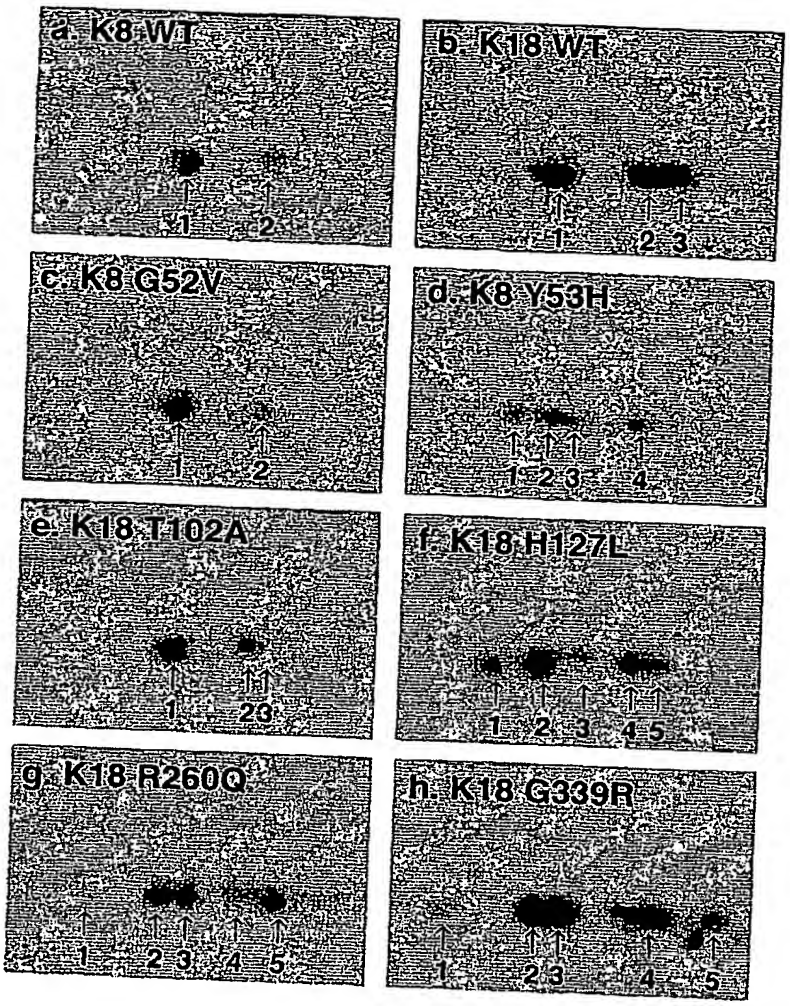
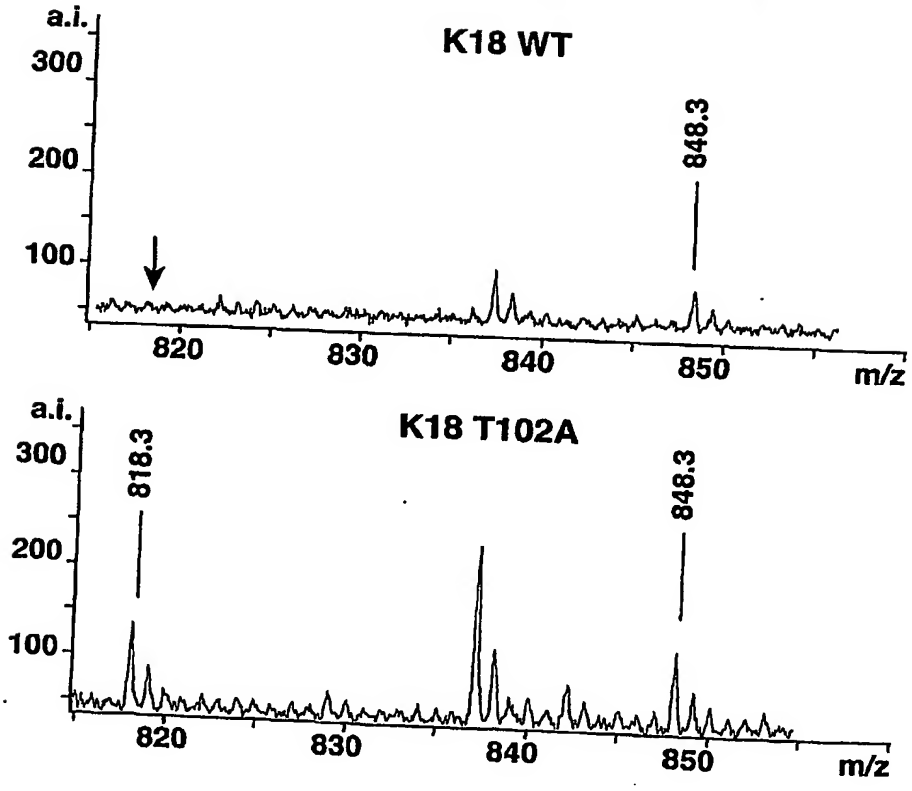

a. K8 WT
1
2
b. K18 WT
1
2 3
c. K8 G52V
1
2
d. K8 Y53H
1 2 3
4
e. K18 T102A
1
2 3
f. K18 H127L
1 2 3 4 5
g. K18 R260Q
1 2 3 4 5
h. K18 G339R
1
2 3
4
5

FIG. 1

B.


a.i.
K18 WT
300
200
100
848.3
820
830
840
850
m/z
a.i.
K18 T102A
300
200
100
818.3
848.3
820
830
840
850
m/z

A.

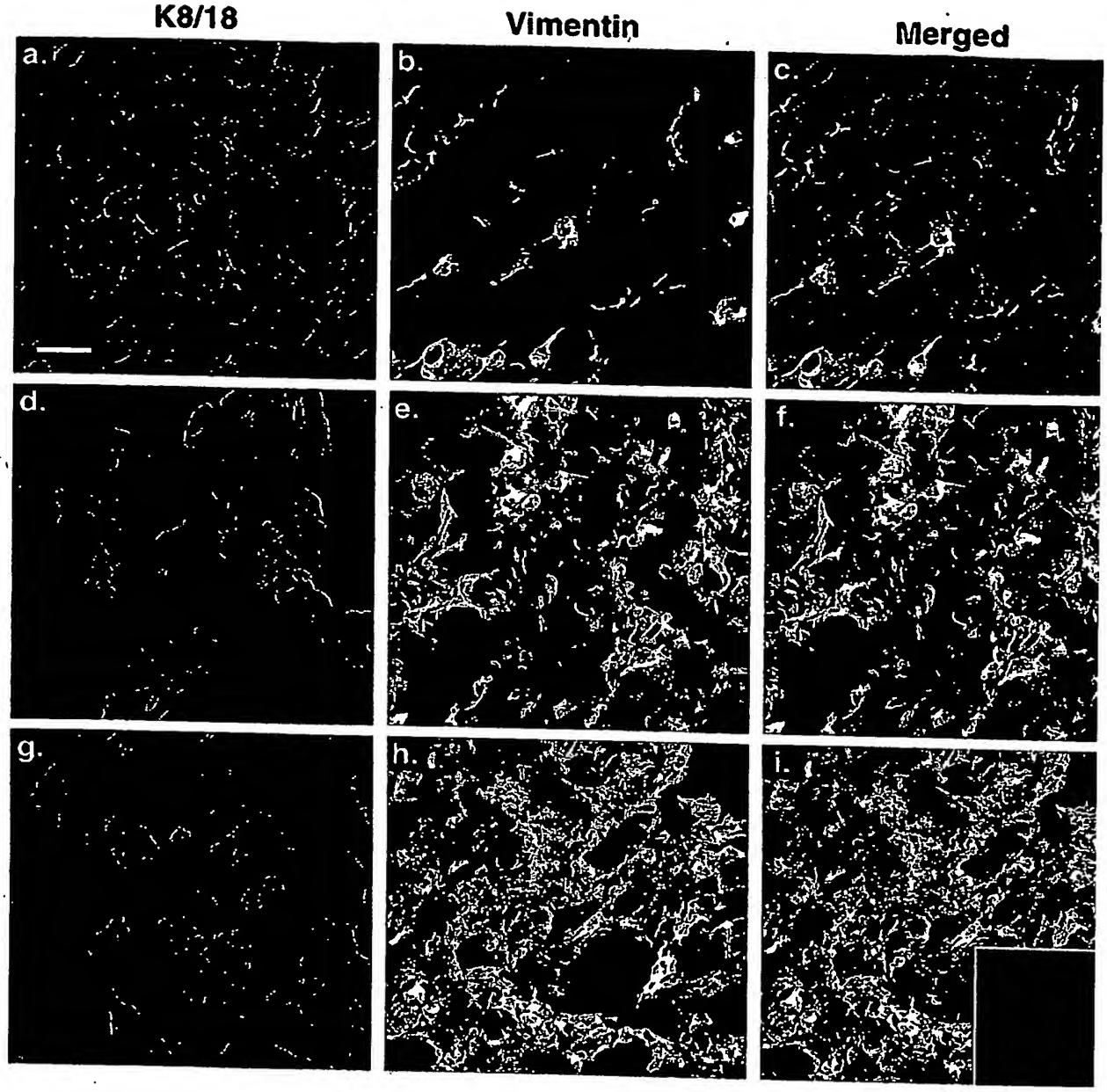
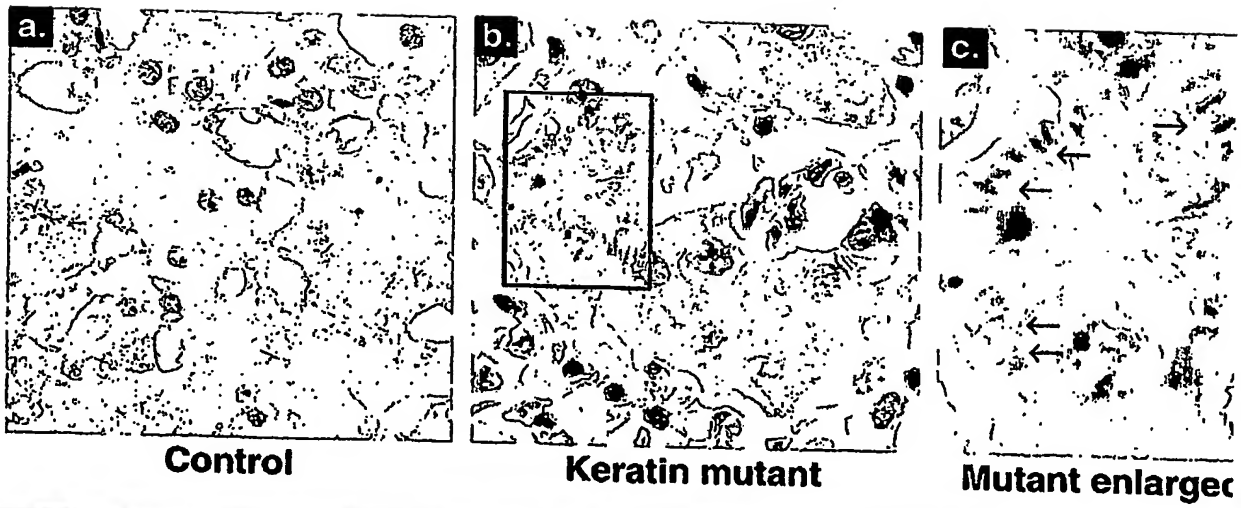

K8/18
Vimentin
Merged
a.
b.
c.
Normal Liver
d.
e.
f.
Acute fulminant hepatitis
g.
h.
i.
Alcoholic cirrhosis (K8 G61C)

FIG. 2

B.


a.
b.
c.
Control
Keratin mutant
Mutant enlarged